

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/816,391

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics  
The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos  
The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length  
The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering  
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII  
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length  
Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 8 ☐ Skipped Sequences (OLD RULES)  
Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:  
**(2) INFORMATION FOR SEQ ID NO:X:**  
**(i) SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
**(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:**  
**This sequence is intentionally skipped**  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES)  
Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.  
**<210> sequence id number**  
**<400> sequence id number**  
**000**
- 10 ☐ Use of n's or Xaa's (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of "Artificial" (NEW RULES)  
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
Valid response is Artificial Sequence.
- 12 ☐ Use of <220>Feature (NEW RULES)  
Sequence(s) ☐ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
**Please explain source of genetic material in <220> to <223> section.**  
**(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)**
- 13 ☐ PatentIn ver. 2.0 "bug"  
**Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/816,391

DATE: 04/09/2001  
TIME: 09:43:22

Input Set : A:\sequence list.txt  
Output Set: N:\CRF3\04092001\I816391.raw

3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
W--> 4 <120> TITLE OF INVENTION: Anaerobic bacterium as a drug for cancer gene therapy  
W--> 5 <130> FILE REFERENCE: DK04F318(US)  
W--> 6 <140> CURRENT APPLICATION NUMBER:  
C--> 7 <141> CURRENT FILING DATE: 2001-03-26  
8 <150> PRIOR APPLICATION NUMBER: JP 00/287688  
W--> 9 <151> PRIOR FILING DATE: 2000-9-21  
W--> 10 <160> NUMBER OF SEQ ID: 3

Does Not Comply  
Corrected Diskette Needed  
pp. 1, 2

## ERRORED SEQUENCES

W--> 11 <210> SEQ ID NO: 1  
12 <211> LENGTH: 600  
13 <212> TYPE: DNA  
14 <213> ORGANISM: Bifidobacterium longum  
W--> 15 <220> FEATURE:  
16 <221> NAME/KEY: CDS  
17 <222> LOCATION: (193)..(471)  
W--> 18 <400> SEQUENCE: 1  
E--> 19 gctgggcgcg gcgcccatga agtggcttga caagcataat cttgtctgat tcgtctatatt  
20 60  
E--> 21 tcaatacctt cggggaaata gatgtgaaaa cccttataaa acgcggggtt tcgcagaaac  
22 120  
E--> 23 atgcgctagt atcattgatg acaacatgga ctaagcaaaa gtgcttgtcc cctgacccaa  
24 180  
E--> 25 gaaggatget tt atg gca tac aac aag tet gac ctc gtt tgc aag atc gcc  
26 231  
27 Met Ala Tyr Asn Lys Ser Asp Leu Val Ser Lys Ile Ala  
W--> 28 1 5 10  
E--> 29 cag aag tcc aac ctg acc aag gct cag gcc gag gct gct gtt aac gcc  
30 279  
31 Gln Lys Ser Asn Leu Thr Lys Ala Gln Ala Glu Ala Ala Val Asn Ala  
W--> 32 15 20 25  
E--> 33 ttc cag gat gtg ttc gtc gag gct atg aag tcc ggc gaa ggc ctg aag  
34 327  
35 Phe Gln Asp Val Phe Val Glu Ala Met Lys Ser Gly Glu Gly Leu Lys  
W--> 37 30 35 40 45  
E--> 38 ctc acc ggc ctg ttc tcc gct gag cgc gtc aag cgc ccg gct cgc acc  
39 375  
W--> 40 Leu Thr Gly Lue Phe Ser Ala Glu Arg Val Lys Arg Pro Ala Arg Thr  
W--> 41 50 55 60  
E--> 42 ggc cgc aac ccg cgc act ggc gag cag att gac att ccg gct tcc tac  
43 423  
44 Gly Arg Asn Pro Arg Thr Gly Glu Gln Ile Asp Ile Pro Ala Ser Tyr  
W--> 46 65 70 75  
E--> 47 ggc gtt cgt atc tcc gct ggc tcc ctg ctg aag aag gcc gtc acc gag  
471

"Wrapped"  
nucleic acid  
numbers. See  
#1 on Error  
Summary sheet.

Invalid amino acid designator

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/816,391

DATE: 04/09/2001

TIME: 09:43:22

Input Set : A:\sequence list.txt

Output Set: N:\CRF3\04092001\I816391.raw

48 (471)  
49 Gly Val Arg Ile Ser Ala Gly Ser Leu Leu Lys Lys Ala Val Thr Glu  
W--> 50 80 85 90  
E--> 51 tgaccttctg ctcgtagcga ttacttcgag cattactgac gacaaagacc ccgaccgaga  
52 (531)  
E--> 53 tggtcgggggt ctttttggtg tgggtgctgtg acgtgttgtc caaccgtatt attccggact  
54 (591)  
E--> 55 agttcagcg  
56 (600)

} "wrapped"  
nucleic acid  
numbers. See  
#1 on the  
Error Summary  
Sheet.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/816,391

DATE: 04/09/2001

TIME: 09:43:23

Input Set : A:\sequence list.txt

Output Set: N:\CRF3\04092001\I816391.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier  
L:5 M:283 W: Missing Blank Line separator, <130> field identifier  
L:6 M:283 W: Missing Blank Line separator, <140> field identifier  
L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:9 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:10 M:283 W: Missing Blank Line separator, <160> field identifier  
L:11 M:283 W: Missing Blank Line separator, <210> field identifier  
L:15 M:283 W: Missing Blank Line separator, <220> field identifier  
L:18 M:283 W: Missing Blank Line separator, <400> field identifier  
L:19 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:1  
M:254 Repeated in SeqNo=1  
L:28 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:32 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:37 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:40 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:41 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:46 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:61 M:283 W: Missing Blank Line separator, <220> field identifier  
L:63 M:283 W: Missing Blank Line separator, <400> field identifier  
L:69 M:283 W: Missing Blank Line separator, <220> field identifier  
L:71 M:283 W: Missing Blank Line separator, <400> field identifier